

# SEQUENCE LISTING

<110> Union Chimique Belge, S.A.  
Nocka, Karl  
Pirozzi, Gregory  
Einstein, Richard

<120> NOVEL GENES ASSOCIATED WITH ALLERGIC HYPERSENSITIVITY AND MAST CELL ACTIVATION

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<170> PatentIn version 3.1

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gac gac gag cgc gag ccc ccg gga ccc cca ggg gcc gcc ccg cca ccg Asp Asp Glu Arg Glu Pro Pro Gly Pro Pro Gly Ala Ala Pro Pro Pro 65 70 75	604
ccc cgc gcc ccg gac gca cag gag ccg gag gag gac gag gcc ggc gcg Pro Arg Ala Pro Asp Ala Gln Glu Pro Glu Glu Asp Glu Ala Gly Ala 80 85 90	652
ggc tgg agc gca gcg ctg cgg gac cgc ccg ccc ccg cgc ttc gag gat Gly Trp Ser Ala Ala Leu Arg Asp Arg Pro Pro Pro Arg Phe Glu Asp 95 100 105	700
acc ggc ggt ccc acc cga aag atg ccc ccc agc gcc agt gcc gtg gac Thr Gly Gly Pro Thr Arg Lys Met Pro Pro Ser Ala Ser Ala Val Asp 110 115 120	748
ttc ttc cag ctc ttt gtc cca gac aac gtc ctc aag aac atg gtg gtg Phe Phe Gln Leu Phe Val Pro Asp Asn Val Leu Lys Asn Met Val Val 125 130 135 140	796
cag aca aac atg tat gcc aag aag ttc cag gag cgg ttt ggg agc gac Gln Thr Asn Met Tyr Ala Lys Lys Phe Gln Glu Arg Phe Gly Ser Asp 145 150 155	844
gga gcc tgg gtg gag gtg acg ctg acg gag atg aag gcg ttc ctg ggc Gly Ala Trp Val Glu Val Thr Leu Thr Glu Met Lys Ala Phe Leu Gly 160 165 170	892
tac atg atc tcc acc agc atc tcc cac tgc gag tcc gtc ctc agc atc Tyr Met Ile Ser Thr Ser Ile Ser His Cys Glu Ser Val Leu Ser Ile 175 180 185	940
tgg agc gga ggc ttc tac agc aac cgc agc ctc gcc ctc gtc atg agc Trp Ser Gly Gly Phe Tyr Ser Asn Arg Ser Leu Ala Leu Val Met Ser 190 195 200	988
cag gcc cgc ttc gag aag atc ctc aag tac ttc cac gtc gtg gcc ttc Gln Ala Arg Phe Glu Lys Ile Leu Lys Tyr Phe His Val Val Ala Phe 205 210 215 220	1036
cgc tcc agc cag acc acg cac ggg ctc tac aag gtc cag ccc ttc ctc Arg Ser Ser Gln Thr Thr His Gly Leu Tyr Lys Val Gln Pro Phe Leu 225 230 235	1084
gac tcc ctg cag aac agc ttc gac tct gcc ttc agg cct tcc caa acc Asp Ser Leu Gln Asn Ser Phe Asp Ser Ala Phe Arg Pro Ser Gln Thr 240 245 250	1132
cag gtg cta cat gaa ccc ctg atc gat gag gat cct gta ttc att gcc Gln Val Leu His Glu Pro Leu Ile Asp Glu Asp Pro Val Phe Ile Ala 255 260 265	1180

acg tgc aca gag cgg gag ctg cga aag agg aaa aag cgg aaa ttc agc	1228
Thr Cys Thr Glu Arg Glu Leu Arg Lys Arg Lys Lys Arg Lys Phe Ser	
270 275 280	
ctc tgg gtc aga caa tgt tct tcc act ggc ttc atc atc cag att tat	1276
Leu Trp Val Arg Gln Cys Ser Ser Thr Gly Phe Ile Ile Gln Ile Tyr	
285 290 295 300	
gtc cac ctg aag gaa ggt ggg ggc cca gat ggc ctg gat gcg ctg aag	1324
Val His Leu Lys Glu Gly Gly Gly Pro Asp Gly Leu Asp Ala Leu Lys	
305 310 315	
aat aag ccc cag ctc cac agc atg gtg gcc agg agc ctg tgc cgg aac	1372
Asn Lys Pro Gln Leu His Ser Met Val Ala Arg Ser Leu Cys Arg Asn	
320 325 330	
gcg gca ggc aag aac tac atc att ttc acg ggg ccc agc atc acc agc	1420
Ala Ala Gly Lys Asn Tyr Ile Ile Phe Thr Gly Pro Ser Ile Thr Ser	
335 340 345	
ctg acg ctg ttt gaa gag ttt gag aag caa ggg att tac tgc tgc ggc	1468
Leu Thr Leu Phe Glu Glu Phe Glu Lys Gln Gly Ile Tyr Cys Cys Gly	
350 355 360	
ttg ctc cgc gcg cgg aag agt gac tgc acc ggc ctc cca ctg tcc atg	1516
Leu Leu Arg Ala Arg Lys Ser Asp Cys Thr Gly Leu Pro Leu Ser Met	
365 370 375 380	
ctg acc aac cca gcc aca ccc ccg gcc cgg ggc cag tac caa atc aag	1564
Leu Thr Asn Pro Ala Thr Pro Pro Ala Arg Gly Gln Tyr Gln Ile Lys	
385 390 395	
atg aag ggg aac atg tcc ttg atc tgc tgg tac aac aaa gga cac ttc	1612
Met Lys Gly Asn Met Ser Leu Ile Cys Trp Tyr Asn Lys Gly His Phe	
400 405 410	
cgc ttc ctg acc aac gcc tac tcc ccg gtg cag cag gga gtc atc atc	1660
Arg Phe Leu Thr Asn Ala Tyr Ser Pro Val Gln Gln Gly Val Ile Ile	
415 420 425	
aaa agg aag agt ggg gag atc cca tgc ccc ttg gcc gtg gag gcg ttt	1708
Lys Arg Lys Ser Gly Glu Ile Pro Cys Pro Leu Ala Val Glu Ala Phe	
430 435 440	
gcc gct cac ctg agc tac atc tgc aga tac gat gac aaa tac agc aag	1756
Ala Ala His Leu Ser Tyr Ile Cys Arg Tyr Asp Asp Lys Tyr Ser Lys	
445 450 455 460	
tat ttc att tct cat aaa cca aac aag acc tgg cag cag gtg ttc tgg	1804
Tyr Phe Ile Ser His Lys Pro Asn Lys Thr Trp Gln Gln Val Phe Trp	
465 470 475	
ttc gcc atc agc atc gcc atc aac aat gcc tac atc ctg tac aaa atg	1852
Phe Ala Ile Ser Ile Ala Ile Asn Asn Ala Tyr Ile Leu Tyr Lys Met	
480 485 490	
tca gac gcc tac cac gtg aag agg tac agc cgg gcg cag ttt gga gag	1900
Ser Asp Ala Tyr His Val Lys Arg Tyr Ser Arg Ala Gln Phe Gly Glu	
495 500 505	
aga ctc gtc aga gag ctg ctg ggc ttg gag gat gcc tct ccg acc cac	1948

Arg	Leu	Val	Arg	Glu	Leu	Leu	Gly	Leu	Glu	Asp	Ala	Ser	Pro	Thr	His	
510						515					520					
tga	tgctgggggc	gcaggactcg	gtcaagggag	gggcaagagg	aggaggagag											2001
cctgccgttc	caacttgccc	atcagagacc	cggacacggc	ctggtgtgtg	gcttgctgcc											2061
tgggagggat	gcacagggcc	tctggaggga	caggatggac	ctggtcagag	gacggttgct											2121
gtcctcattt	gcattccaag	aagagcatgt	cctccctcga	gaaacagtgc	cgccgggtgtg											2181
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ttactgttgc	ttcagatcta	atgtaaaagg	cagatgtccc	ctcctctcca	ccccgacgc											2721
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tgtctttcct	ctgtgtgtag	tgagtgacct	tggcagtggt	tgctgtctca	gagtggcccc											3021
tcagaacaac	agggctggcc	ttggaaaaac	cccaaaacag	gactgtgggtg	acaactctgg											3081
tcaggtgtga	tttgacatga	gggccggagg	cggttgctga	cggcaggact	ggagaggctg											3141
cgtgcccggc	actggcagcg	aggctcgtgt	gtcccccagg	cagatctggg	cactttccca											3201
accaggtttt	atgctgtctc	agggaagcct	cggtgccaga	gtggtgggca	gatctgacca											3261
tccccacaga	ccagaaacaa	ggaattttctg	ggattaccca	gtcccccttc	aaccagttg											3321
atgtaaccac	ctcatTTTTT	acaaatacag	aatctattct	actcaggcta	tgggcctcgt											3381
cctcactcag	ttattgagag	tgttgctgtc	cgcattgtcc	gggccccacg	tggctcctgt											3441
gctctagatc	atggtgactc	ccccgccctg	tggttggaat	cgatgccacg	gattgcaggc											3501
caaatttcag	atcgtgtttc	caaacaccct	tgctgtgccc	tttaatggga	ttgaaagcac											3561
ttttaccaca	tggagaaata	tatttttaat	ttgtgatgct	tttctacaag	gtccactatt											3621
tctgagttta	atgtgtttcc	aacacttaag	gagactctaa	tgaaagctga	tgaattttct											3681

tttctgtcca aacaagtaaa ataaaaataa aagtctatatt agatgttaaa aaaaaaaaaa 3741

aa 3743

<210> 7  
<211> 524  
<212> PRT  
<213> Homo sapiens

<400> 7

Met Ala Glu Gly Gly Gly Gly Ala Arg Arg Arg Ala Pro Ala Leu Leu  
1 5 10 15

Glu Ala Ala Arg Ala Arg Tyr Glu Ser Leu His Ile Ser Asp Asp Val  
20 25 30

Phe Gly Glu Ser Gly Pro Asp Ser Gly Gly Asn Pro Phe Tyr Ser Thr  
35 40 45

Ser Ala Ala Ser Arg Ser Ser Ser Ala Ala Ser Ser Asp Asp Glu Arg  
50 55 60

Glu Pro Pro Gly Pro Pro Gly Ala Ala Pro Pro Pro Pro Arg Ala Pro  
65 70 75 80

Asp Ala Gln Glu Pro Glu Glu Asp Glu Ala Gly Ala Gly Trp Ser Ala  
85 90 95

Ala Leu Arg Asp Arg Pro Pro Pro Arg Phe Glu Asp Thr Gly Gly Pro  
100 105 110

Thr Arg Lys Met Pro Pro Ser Ala Ser Ala Val Asp Phe Phe Gln Leu  
115 120 125

Phe Val Pro Asp Asn Val Leu Lys Asn Met Val Val Gln Thr Asn Met  
130 135 140

Tyr Ala Lys Lys Phe Gln Glu Arg Phe Gly Ser Asp Gly Ala Trp Val  
145 150 155 160

Glu Val Thr Leu Thr Glu Met Lys Ala Phe Leu Gly Tyr Met Ile Ser  
165 170 175

Thr Ser Ile Ser His Cys Glu Ser Val Leu Ser Ile Trp Ser Gly Gly  
180 185 190

Phe Tyr Ser Asn Arg Ser Leu Ala Leu Val Met Ser Gln Ala Arg Phe

100059001 20650001

195	200	205																	
Glu Lys Ile Leu Lys Tyr Phe His Val Val Ala Phe Arg Ser Ser Gln																			
210	215	220																	
Thr Thr His Gly Leu Tyr Lys Val Gln Pro Phe Leu Asp Ser Leu Gln																			
225	230	235																	240
Asn Ser Phe Asp Ser Ala Phe Arg Pro Ser Gln Thr Gln Val Leu His																			
	245	250																	255
Glu Pro Leu Ile Asp Glu Asp Pro Val Phe Ile Ala Thr Cys Thr Glu																			
	260	265																	270
Arg Glu Leu Arg Lys Arg Lys Lys Arg Lys Phe Ser Leu Trp Val Arg																			
	275	280																	285
Gln Cys Ser Ser Thr Gly Phe Ile Ile Gln Ile Tyr Val His Leu Lys																			
	290	295																	300
Glu Gly Gly Gly Pro Asp Gly Leu Asp Ala Leu Lys Asn Lys Pro Gln																			
305	310	315																	320
Leu His Ser Met Val Ala Arg Ser Leu Cys Arg Asn Ala Ala Gly Lys																			
	325	330																	335
Asn Tyr Ile Ile Phe Thr Gly Pro Ser Ile Thr Ser Leu Thr Leu Phe																			
	340	345																	350
Glu Glu Phe Glu Lys Gln Gly Ile Tyr Cys Cys Gly Leu Leu Arg Ala																			
	355	360																	365
Arg Lys Ser Asp Cys Thr Gly Leu Pro Leu Ser Met Leu Thr Asn Pro																			
	370	375																	380
Ala Thr Pro Pro Ala Arg Gly Gln Tyr Gln Ile Lys Met Lys Gly Asn																			
385	390	395																	400
Met Ser Leu Ile Cys Trp Tyr Asn Lys Gly His Phe Arg Phe Leu Thr																			
	405	410																	415
Asn Ala Tyr Ser Pro Val Gln Gln Gly Val Ile Ile Lys Arg Lys Ser																			
	420	425																	430
Gly Glu Ile Pro Cys Pro Leu Ala Val Glu Ala Phe Ala Ala His Leu																			
	435	440																	445

Ser Tyr Ile Cys Arg Tyr Asp Asp Lys Tyr Ser Lys Tyr Phe Ile Ser  
 450 455 460

His Lys Pro Asn Lys Thr Trp Gln Gln Val Phe Trp Phe Ala Ile Ser  
 465 470 475 480

Ile Ala Ile Asn Asn Ala Tyr Ile Leu Tyr Lys Met Ser Asp Ala Tyr  
 485 490 495

His Val Lys Arg Tyr Ser Arg Ala Gln Phe Gly Glu Arg Leu Val Arg  
 500 505 510

Glu Leu Leu Gly Leu Glu Asp Ala Ser Pro Thr His  
 515 520

<210> 8  
 <211> 1998  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (162)..(635)  
 <223> 1st open reading frame

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 gcttcctaac tcatttttga ataatactag gctacaaaga attacactgt gaattcatta 120  
 agggtaacac caaatcacta aacagcactg tttgtacaga a atg tcg aaa agc tgt 176  
 Met Ser Lys Ser Cys  
 1 5  
 gga aat aat tta gcg gcc att tct gta gga att tcg ctt ctt tta ctc 224  
 Gly Asn Asn Leu Ala Ala Ile Ser Val Gly Ile Ser Leu Leu Leu Leu  
 10 15 20  
 tta gtg gtt tgt gga att ggg tgt gtt tgg cac tgg aaa cac cgt gtt 272  
 Leu Val Val Cys Gly Ile Gly Cys Val Trp His Trp Lys His Arg Val  
 25 30 35  
 gcc aca cga ttt acc tta ccg agg ttt tta caa agg aga agc agc agg 320  
 Ala Thr Arg Phe Thr Leu Pro Arg Phe Leu Gln Arg Arg Ser Ser Arg  
 40 45 50  
 aga aaa gtc tgt act aaa aca ttc ttg ggc ccc cgc atc att ggc tta 368  
 Arg Lys Val Cys Thr Lys Thr Phe Leu Gly Pro Arg Ile Ile Gly Leu  
 55 60 65  
 agg cat gaa atc tca gtt gaa acc caa gac cac aaa tct gct gtc agg 416  
 Arg His Glu Ile Ser Val Glu Thr Gln Asp His Lys Ser Ala Val Arg  
 70 75 80 85



gga aat aac aca cac gac aac tat gaa aat gtg gaa gca ggt cct ccc	464
Gly Asn Asn Thr His Asp Asn Tyr Glu Asn Val Glu Ala Gly Pro Pro	
90 95 100	
aaa gct aaa gga aaa acc gat aag gaa cta tat gaa aac aca ggg cag	512
Lys Ala Lys Gly Lys Thr Asp Lys Glu Leu Tyr Glu Asn Thr Gly Gln	
105 110 115	
tct aat ttc gag gag cat atc tat gga aat gag aca tct tct gac tat	560
Ser Asn Phe Glu Glu His Ile Tyr Gly Asn Glu Thr Ser Ser Asp Tyr	
120 125 130	
tat aac ttc cag aag cct cgt cct tct gaa gtt cct caa gat gaa gat	608
Tyr Asn Phe Gln Lys Pro Arg Pro Ser Glu Val Pro Gln Asp Glu Asp	
135 140 145	
ata tac att ctt cca gat tca tat tag cttttcaaaa tattgacttt	655
Ile Tyr Ile Leu Pro Asp Ser Tyr	
150 155	
tgttattgga tgataaatat tcaactgtaat ttttcaacag caaagacaag gaatcaaact	715
aaatgttgat caactgtaga ctggataaag aaaatgtggt acacatacac catagaatat	775
tatgcagccg taaaaaaaga acaaaactaa catgggaaca gaaaatcaaa taccacatat	835
tctcacttaa aagtgggagc taaataataa gaacacatgg agagaaggag aggaacaaca	895
gacactgggg cctacttgag ggaggacagt ggaaggaggg agagggttcag ggaaaaaaaa	955
aatatcaggt actatgctta gtacacacat gatgaaataa tctgtacacc aaacccccaa	1015
gtcacaagtg ttctacata acaaacctga acatgtaccc ctgaacataa aattataatt	1075
aaaatattaa aaataattca ctgtgatttt tattgtactg atgccattct taatcaagtt	1135
ctgataagtg gatggtctct gcctatctcc acctttctga atcctatgtg tatcgctgtg	1195
gattaattct agatatcttc tccaccctcc ttgcaccaga ctaaactctgt attatgtgat	1255
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tatctggctc agaattattg tcataggctc ctaactgttc ctctgcttc tagtttctac	1375
ccactcaatc aattaccgat ggtgttgcca gatttatctt cagaaaatat tcctaacagc	1435
cacattattt ctttcaacta aaatgtttta atgccccctc tttgcaaaag acataatacc	1495
cataatttga actccaaaat ttatggtttt ccacaattgg ttccaattca cttttccagt	1555
gacttctctt actatctctc atttctttgc cttcagcaga atcatcttaa aacctgccaa	1615
acttatcctt ccttcacagc tttgcttttc tgccctcttct ctcaagcctg cttcagatca	1675
taagttcttc cacacatctc ctgaatcact ccaaaccgc atttaccttt ttattttctg	1735
atataagctt tgatgcctct tcaattotta ggacatttaa acatatgaat gttgccacag	1795
cattttatta cctagcttca tatgaaaatg tcttaaattc ccacctaaat gaaaagaaac	1855

tgcccaaattg cctagaacat cacataaggc actaaatgcc tcatgtttta ctgacgggaa 1915  
 ttgaattgta cattttgctg agtagttttg agaaaaaat ctaataaatt catctgttat 1975  
 tcatccataa aaaaaaaaaa aaa 1998

<210> 9  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 9

Met Ser Lys Ser Cys Gly Asn Asn Leu Ala Ala Ile Ser Val Gly Ile  
 1 5 10 15

Ser Leu Leu Leu Leu Val Val Cys Gly Ile Gly Cys Val Trp His  
 20 25 30

Trp Lys His Arg Val Ala Thr Arg Phe Thr Leu Pro Arg Phe Leu Gln  
 35 40 45

Arg Arg Ser Ser Arg Arg Lys Val Cys Thr Lys Thr Phe Leu Gly Pro  
 50 55 60

Arg Ile Ile Gly Leu Arg His Glu Ile Ser Val Glu Thr Gln Asp His  
 65 70 75 80

Lys Ser Ala Val Arg Gly Asn Asn Thr His Asp Asn Tyr Glu Asn Val  
 85 90 95

Glu Ala Gly Pro Pro Lys Ala Lys Gly Lys Thr Asp Lys Glu Leu Tyr  
 100 105 110

Glu Asn Thr Gly Gln Ser Asn Phe Glu Glu His Ile Tyr Gly Asn Glu  
 115 120 125

Thr Ser Ser Asp Tyr Tyr Asn Phe Gln Lys Pro Arg Pro Ser Glu Val  
 130 135 140

Pro Gln Asp Glu Asp Ile Tyr Ile Leu Pro Asp Ser Tyr  
 145 150 155

<210> 10  
 <211> 1998  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> (373)..(651)  
 <223> 2nd open reading frame

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 agggtaacac caaatcacta aacagcactg tttgtacaga aatgtcgaaa agctgtggaa 180  
 ataatttagc ggccatttct gtaggaattt cgcttctttt actcttagtg gtttgtggaa 240  
 ttgggtgtgt ttggcactgg aaacaccgtg ttgccacacg atttacctta ccgaggtttt 300  
 tacaaaggag aagcagcagg agaaaagtct gtactaaaac attcttgggc ccccgcatca 360  
 ttggcttaag gc atg aaa tct cag ttg aaa ccc aag acc aca aat ctg ctg 411  
                   Met Lys Ser Gln Leu Lys Pro Lys Thr Thr Asn Leu Leu  
                   1                  5                  10  
 tca ggg gaa ata aca cac acg aca act atg aaa atg tgg aag cag gtc 459  
 Ser Gly Glu Ile Thr His Thr Thr Thr Met Lys Met Trp Lys Gln Val  
                   15                  20                  25  
 ctc cca aag cta aag gaa aaa ccg ata agg aac tat atg aaa aca cag 507  
 Leu Pro Lys Leu Lys Glu Lys Pro Ile Arg Asn Tyr Met Lys Thr Gln  
                   30                  35                  40                  45  
 ggc agt cta att tcg agg agc ata tct atg gaa atg aga cat ctt ctg 555  
 Gly Ser Leu Ile Ser Arg Ser Ile Ser Met Glu Met Arg His Leu Leu  
                   50                  55                  60  
 act att ata act tcc aga agc ctc gtc ctt ctg aag ttc ctc aag atg 603  
 Thr Ile Ile Thr Ser Arg Ser Leu Val Leu Leu Lys Phe Leu Lys Met  
                   65                  70                  75  
 aag ata tat aca ttc ttc cag att cat att agc ttt tca aaa tat tga 651  
 Lys Ile Tyr Thr Phe Phe Gln Ile His Ile Ser Phe Ser Lys Tyr  
                   80                  85                  90  
 cttttgttat tggatgataa atattcactg taatttttca acagcaaaga caaggaatca 711  
 aactaaatgt tgatcaactg tagactggat aaagaaaatg tggtagacat acaccataga 771  
 atattatgca gccgtaaaaa aagaacaaaa ctaacatggg aacagaaaat caaataccac 831  
 atattctcac ttaaaagtgg gagctaaata ataagaacac atggagagaa ggagaggaac 891  
 aacagacact ggggcctact tgagggagga cagtggaagg agggagaggt tcagggaaaa 951  
 aaaaaatatt aggtactatg cttagtacac acatgatgaa ataactctgta caccaaacc 1011  
 ccaagtcaca agtgttccta cataacaaac ctgaacatgt acccctgaac ataaaattat 1071  
 aattaaata ttaaaaataa ttcactgtga tttttattgt actgatgcca ttcttaatca 1131  
 agttctgata agtggatggg ctctgcctat ctccaccttt ctgaatccta tgtgtatcgc 1191  
 tgtggattaa ttctagatat cttctccacc ctccctgcac cagactaaat ctgtattatg 1251

tgatattgat tcttccttct aaatattacc cgttatctct ttcctttatt tctaccatta 1311  
tctttatctg gctcagaatt attgtcatag gctcctaact gttcctcctg cttctagttt 1371  
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cagccacatt atttctttca cttaaaatgt tttaatgccc cctctttgca aaagacataa 1491  
taccataat ttgaactcca aaatttatgg tttccacaaa ttggttccaa ttcacttttc 1551  
cagtgacttc tcttactatc tctcatttct ttgccttcag cagaatcatc ttaaaacctg 1611  
ccaaacttat ccttccttca cagctttgct tttctgcctc ttctctcaag cctgcttcag 1671  
atcataagtt cttccacaca tctcctgaat cactccaaac ccgcatttac ctttttattt 1731  
tctgatataa gctttgatgc ctcttcaatt cttaggacat ttaaacadat gaatgttgcc 1791  
acagcatttt attacctagc ttcatatgaa aatgtcttaa attcccacct aaatgaaaag 1851  
aaactgccca aatgcctaga acatcacata aggcaactaaa tgctcatgt tttactgacg 1911  
ggaattgaat tgtacatttt gctgagtagt tttgagaaaa aaatctaata aattcatctg 1971  
ttattcatcc ataaaaaaaa aaaaaaa 1998

<210> 11  
<211> 92  
<212> PRT  
<213> Homo sapiens  
<400> 11

Met Lys Ser Gln Leu Lys Pro Lys Thr Thr Asn Leu Leu Ser Gly Glu  
1 5 10 15

Ile Thr His Thr Thr Thr Met Lys Met Trp Lys Gln Val Leu Pro Lys  
20 25 30

Leu Lys Glu Lys Pro Ile Arg Asn Tyr Met Lys Thr Gln Gly Ser Leu  
35 40 45

Ile Ser Arg Ser Ile Ser Met Glu Met Arg His Leu Leu Thr Ile Ile  
50 55 60

Thr Ser Arg Ser Leu Val Leu Leu Lys Phe Leu Lys Met Lys Ile Tyr  
65 70 75 80

Thr Phe Phe Gln Ile His Ile Ser Phe Ser Lys Tyr  
85 90

<210> 12  
<211> 1662  
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1662)

<223>

<400> 12

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Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala	
1 5 10 15	

cag ctc ttg ctg gtc aac ctg cta acc ttt ggc ctg gag gtg tgt ttg	96
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu	
20 25 30	

gcc gca ggc atc acc tat gtg ccg cct ctg ctg ctg gaa gtg ggg gta	144
Ala Ala Gly Ile Thr Tyr Val Pro Leu Leu Leu Glu Val Gly Val	
35 40 45	

gag gag aag ttc atg acc atg gtg ctg ggc att ggt cca gtg ctg ggc	192
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly	
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ctg gtc tgt gtc ccg ctc cta ggc tca gcc agt gac cac tgg cgt gga	240
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly	
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cgc tat ggc cgc cgc cgg ccc ttc atc tgg gca ctg tcc ttg ggc atc	288
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile	
85 90 95	

ctg ctg agc ctc ttt ctc atc cca agg gcc ggc tgg cta gca ggg ctg	336
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu	
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ctg tgc ccg gat ccc agg ccc ctg gag ctg gca ctg ctc atc ctg ggc	384
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly	
115 120 125	

gtg ggg ctg ctg gac ttc tgt ggc cag gtg tgc ttc act cca ctg gag	432
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu	
130 135 140	

gcc ctg ctc tct gac ctc ttc cgg gac ccg gac cac tgt cgc cag gcc	480
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala	
145 150 155 160	

tac tct gtc tat gcc ttc atg atc agt ctt ggg ggc tgc ctg ggc tac	528
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr	
165 170 175	

ctc ctg cct gcc att gac tgg gac acc agt gcc ctg gcc ccc tac ctg	576
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu	
180 185 190	

ggc acc cag gag gag tgc ctc ttt ggc ctg ctc acc ctc atc ttc ctc	624
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu	
195 200 205	

acc tgc gta gca gcc aca ctg ctg gtg gct gag gag gca gcg ctg ggc Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly 210 215 220	672
ccc acc gag cca gca gaa ggg ctg tcg gcc ccc tcc ttg tcg ccc cac Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His 225 230 235 240	720
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cgg ctc ttc gtg gct gag ctg tgc agc tgg atg gca ctc atg acc ttc Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe 275 280 285	864
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tcc ctc tac cac cgg gag aag cag gtg ttc ctg ccc aaa tac cga ggg Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly 405 410 415	1248
gac act gga ggt gct agc agt gag gac agc ctg atg acc agc ttc ctg Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu 420 425 430	1296
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gga ggc agt ggc ctg ctc cca cct cca ccc gcg ctc tgc ggg gcc tct	1392

Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser  
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gcc tgt gat gtc tcc gta cgt gtg gtg gtg ggt gag ccc acc gag gcc 1440  
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Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
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Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val  
35 40 45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
50 55 60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
65 70 75 80

Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
85 90 95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
100 105 110





Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
355 360 365

Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
370 375 380

Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
405 410 415

Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
420 425 430

Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
435 440 445

Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser  
450 455 460

Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
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Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
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Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
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Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
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Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp  
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Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
545 550